

# Genetic Resources Conservation and Strategies for Enhanced Utilization in Crop Improvement

HD Upadhyaya, S Sharma, SL Dwivedi, S Singh, RK Varshney, M Vetriventhan, SK Pattanashetti and N Lalitha

## Background

Global food production will need to double to feed the more than 9 billion people by 2050. To address this enormous challenge, the development of better adapted, higher yielding, and resource-use-efficient crop cultivars is crucial. The effective utilization of plant genetic resources in breeding is the most sustainable way to increase food production while conserving biodiversity (Table 1).

Crop	Number of accessions conserved			Number of samples distributed		
	Cultivated	Wild	Total	India	Other Countries	ICRISAT
Sorghum	37,491	458	37,949 (92)*	131,175	131,166 (108)	240,028
Pearl millet	21,908	750	22,658 (50)	62,002	34,943 (80)	55,634
Chickpea	19,960	308	20,268 (60)	73,598	58,594 (87)	190,030
Pigeonpea	13,216	555	13,771 (74)	50,336	22,036 (111)	84,593
Groundnut	14,968	478	15,446 (92)	47,507	51,924 (95)	97,433
Small millets (6)	10,104	258	10,362 (50)	43,051	21,362 (60)	7,906

\*Figures in parenthesis refer to number of countries

## Seed Conservation Strategies

**Short-term:** 18-20°C and 30-40% relative humidity (RH)

**Medium-term (active collection):** 4°C and 30% relative humidity (RH); Seed viability: above 85% for 15-20 years.

**Long-term (Base collection):** -20°C; seed viability above 85% for 50 years or more.

## Safety Back-up at Svalbard Global Seed Vault

To date, we have contributed seed samples of 104,000 unique accessions of chickpea, groundnut, pigeonpea, pearl millet and sorghum and of six small millets for safety duplication at Svalbard Global Seed Vault, Norway.

## Low Use of Germplasm – A Major Concern in Crop Breeding

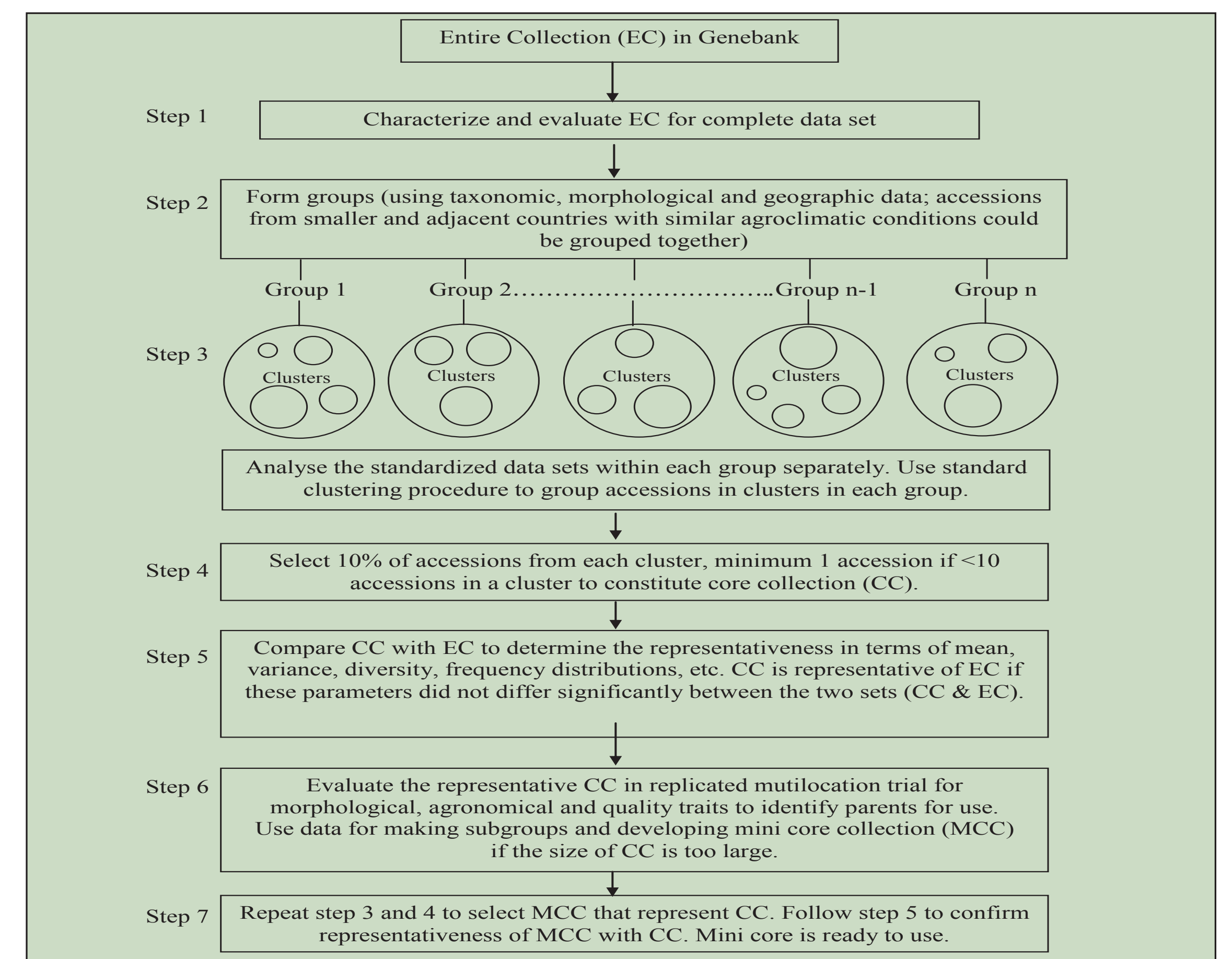
Managing and utilizing such large diversity is the greatest challenge to germplasm curators and crop breeders. Less than 1% of germplasm has been used in crop improvement. Promoting the use of germplasm in crop improvement programs is a major concern as breeders are reluctant to use germplasm largely either due to lack of reliable information on economic traits besides linkage drag or due to breakdown of co-adapted gene complexes.

## Means to Overcome Low Use of Germplasm in Crop Breeding

### Developing Core and Mini Core Collections to Enhance Use of Germplasm in Crop Breeding

Core and/or mini core collections, using passport, characterization and evaluation data have been formed in chickpea, groundnut, pigeonpea, pearl millet, sorghum, and six small millets (Table 2).

Crop	Forming reduced subsets		
	Core collection	Mini core collection	Reference set
Barnyard millet	89		
Chickpea	1,956	211	300
Finger millet	622	80	300
Foxtail millet	155	35	200
Groundnut	1,704	184	300
Kodo millet	75		
Little millet	56		
Pearl millet	2,094	238	300
Pigeonpea	1,290	146	300
Proso millet	106		
Sorghum	2,247	242	383



Flow diagram to establish core and mini core collections in a crop

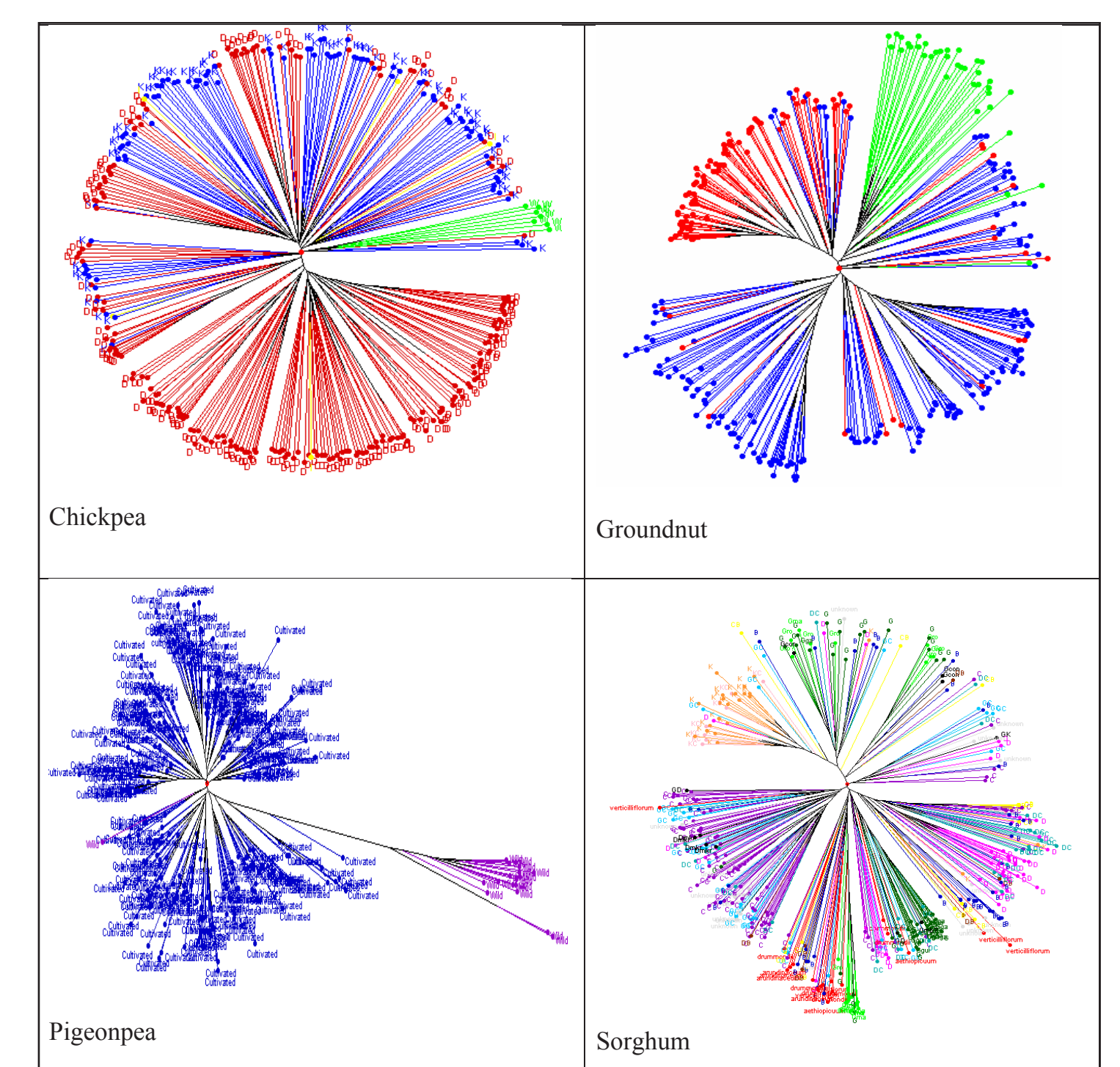
## Multi-trait Genetically Diverse Germplasm for Use in Crop Improvement

Researchers at ICRISAT and elsewhere have extensively evaluated mini core collections and identified several sources of resistances to abiotic and biotic stresses, including some with specific adaptation having multiple resistances and/or seed nutrient dense types. Genotyping information was used to identify agronomically beneficial and genetically diverse germplasm pairs in most of our crops for use in crop breeding.

## Population Structure, Diversity and Association Genetics in Germplasm Collections

Advances in genomics on these crops are now assisting us to dissect population structure, diversity, and marker-trait associations for agronomically beneficial traits using genome-wide association mapping, i.e., SSRs and SNPs associated with flowering and maturity, tillers, plant height, inflorescence architecture, seed weight, and resistance to anthracnose, grain mold and rust in sorghum.

Similar studies are in progress in chickpea and groundnut, providing opportunities for crop improvement through marker-assisted breeding and genomic selection.



## Pre-breeding to Access Novel Alleles from Wild Relatives

Wild relatives possessing resistance to pest and diseases have been crossed with cultivated types to transfer resistance to major pest and diseases in cultigen's gene pools of chickpea, groundnut and pigeonpea. Groundnut and chickpea lines with improved seed yield and seed size have been developed using wild relatives.

